

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2004, 16:36:47 ; Search time 0.001 Seconds

(without alignments)
34.620 Million cell updates/sec

Title: us-09-954-556-3

Perfect score: 30

Sequence: 1 cagcacaagaagccagacttcagcagcca 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 44 seqs, 577 residues

Total number of hits satisfying chosen parameters: 88

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 44 summaries

Database : rn1.seq *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.4	48.0	17	1	US-08-541-950B-17
2	14.4	48.0	17	1	US-08-541-950B-20
3	14.4	48.0	17	1	US-09-083-756A-17
4	14.4	48.0	17	1	US-09-083-756A-20
5	14.4	48.0	18	1	US-08-541-950B-23
6	14.4	48.0	18	1	US-09-083-756A-23
7	13.8	46.0	17	1	US-09-325-601-1
8	13.8	46.0	18	1	US-08-541-950B-13
9	13.8	46.0	18	1	US-09-083-756A-13
10	13.8	46.0	18	1	US-09-325-601-3
11	12.8	42.7	17	1	US-08-541-950B-18
12	12.8	42.7	17	1	US-08-541-950B-19
13	12.8	42.7	17	1	US-08-541-950B-21
14	12.8	42.7	17	1	US-08-541-950B-22
15	12.8	42.7	17	1	US-09-083-756A-18
16	12.8	42.7	17	1	US-09-083-756A-19
17	12.8	42.7	17	1	US-09-083-756A-21
18	12.8	42.7	17	1	US-09-083-756A-22
19	11.8	39.3	15	1	US-08-363-240A-47
20	11.4	36.0	15	1	US-08-050-073-65
21	9.4	31.3	12	1	US-09-281-418-65
22	9	30.0	10	1	US-09-508-753B-25
23	8.4	28.0	10	1	US-09-263-790-35
24	8.4	28.0	10	1	US-09-721-777-18
25	8.4	28.0	10	1	US-08-545-253A-20
26	8.4	28.0	10	1	US-08-719-337-20
27	8.4	28.0	10	1	US-08-878-835A-12
28	8.4	28.0	10	1	US-09-508-753B-28
29	8.4	28.0	10	1	US-09-508-753B-63
30	8.4	28.0	10	1	US-08-894-454-110
31	8.4	28.0	10	1	US-09-758-073-6
32	8.4	28.0	10	1	US-08-173-489C-342
33	8.4	28.0	11	1	US-08-173-489C-342

C 34	8.4	28.0	11	1	US-09-862-847-15	Sequence 15, Appl
C 35	8	26.7	8	1	US-08-859-954-95	Sequence 95, Appl
C 36	8	26.7	8	1	US-09-041-675-19	Sequence 19, Appl
C 37	8	26.7	8	1	US-09-041-675-24	Sequence 24, Appl
C 38	8	26.7	9	1	US-09-989-789-455	Sequence 455, App
C 39	8	26.7	9	1	US-09-989-789-456	Sequence 456, App
C 40	8	26.7	10	1	US-08-060-952C-9	Sequence 9, Appl
C 41	8	26.7	10	1	US-08-997-897-4	Sequence 4, Appl
C 42	8	26.7	10	1	US-09-156-836B-4	Sequence 4, Appl
C 43	8	26.7	10	1	US-08-464-011B-9	Sequence 9, Appl
C 44	8	26.7	10	1	US-09-336-946B-15	Sequence 15, Appl

ALIGNMENTS

```
RESULT 1
US-08-541-950B-17
; Sequence 17, Application US/08541950B
; Patent No. 5821046
; GENERAL INFORMATION:
; APPLICANT: Karm J, Galt MJ, Heaphy S, Dingwall C
; TITLE OF INVENTION: VIRAL (HIV) GROWTH INHIBITION
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: One Financial Center, 45th Floor
; CITY: Boston
; STATE: MA
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,950B
; FILING DATE: 10/10/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/960,370
; FILING DATE: 03/19/93
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: synthetic RNA
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 8
; OTHER INFORMATION: N is 2'-deoxythymidine
; US-08-541-950B-17

Query Match 48.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.9;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 1490 AGCCAGACTTCAGCAGC 1506
Db 1 AGCCAGANTUGAGCAGC 17

RESULT 2
US-08-541-950B-20
; Sequence 20, Application US/08541950B
```

107	8.4	28.0	10	1	AAE34426	Yeast NORF gene SA
C 108	8.4	28.0	10	1	AAE34234	Yeast NORF gene SA
109	8.4	28.0	10	1	AAE19669	Primer-extension o
110	8.4	28.0	10	1	ABE52200	Human PER1 preter
C 111	8.4	28.0	10	1	ABK81399	SCY21 gene primer
C 112	8.4	28.0	10	1	ABK96063	Human LIPE gene po
C 113	8.4	28.0	10	1	AAE25204	Human homeo box D3
C 114	8.4	28.0	10	1	ABV64823	Human haemopexin S
C 115	8.4	28.0	10	1	ABK54423	Human ISL1 gene AS
C 116	8.4	28.0	10	1	ABK11491	Oligonucleotide pr
117	8.4	28.0	10	1	ABK72629	Leukotriene B4 rec
C 118	8.4	28.0	10	1	ACA94480	DNA tag from human
C 119	8.4	28.0	10	1	ABT14411	Nucleic acid PCR a
C 120	8.4	28.0	10	1	ABT14333	Nucleic acid PCR a
C 121	8.4	28.0	11	1	AAK14955	Triple helix third
C 122	8.4	28.0	11	1	ABO86554	Human skin stress/
C 123	8.4	28.0	11	1	ABO86306	Human skin stress/
C 124	8.4	28.0	11	1	ABO87206	Human skin stress/
C 125	8.4	28.0	11	1	ABV64744	Human skin EST 253
C 126	8.4	28.0	11	1	ABV67763	Human skin EST 554
C 127	8.4	28.0	11	1	ABV69450	Human skin EST 723
C 128	8.4	28.0	11	1	ABV69082	Human skin EST 686
C 129	8.4	28.0	11	1	ABV66542	Human skin EST 413
C 130	8.4	28.0	11	1	ABV66542	Human skin EST 432
C 131	8.4	28.0	11	1	ABV66760	Human skin EST 454
C 132	8.4	28.0	11	1	ABV68413	Human skin EST 619
C 133	8.4	28.0	11	1	ABV69080	Human skin EST 686
C 134	8.4	28.0	11	1	ABV68371	Human skin EST 615
C 135	8.4	28.0	11	1	ABV68621	Human skin EST 640
C 136	8.4	28.0	11	1	ABV63846	Human skin EST 163
C 137	8.4	28.0	11	1	ABV65219	Human skin EST 300
C 138	8.4	28.0	11	1	ABV66909	Human skin EST 469
C 139	8.4	28.0	11	1	ABV71267	Human skin EST 905
C 140	8.4	28.0	11	1	ABV67181	Human skin EST 496
C 141	8.4	28.0	11	1	ABV66102	Human skin EST 388
C 142	8.4	28.0	11	1	AAE21210	Transmissible gast
C 143	8.4	28.0	11	1	ABT16435	Human neurokinin 1

ALIGNMENTS

RESULT 1
ID AAQ24060 standard; RNA, 17 BP.

AC AAQ24060;
08-JUN-1992 (first entry)

DE Artificial HIV-1 TAR sequence containing U-rich bubble.

XX human immunodeficiency virus; tat protein; AIDS; hairpin loop;
KW trans-activation responsive region; ss.
XX Synthetic.

XX Key Location/Qualifiers
FH misc_structure 5..12
FT /tag= a
FT /note= "U-rich bubble. Base pairs to nucleotides 6-10 of
AAQ24061"

XX W09202228-A.
XX PD 20-FEB-1992.
XX 02-AUG-1990; 90GB-00016973.
XX 02-AUG-1990; 90GB-00016973.
(MED1-) MED RES COUNCIL.

PI Karn J, Gait MJ, Heaphy S, Dingwall C;
XX WPI, 1992-079785/10.
DR
XX New HIV growth inhibiting oligo:nucleotide(s) - comprising rna binding
PT sequences capable of binding to tat protein within cells, and in assays
PT to identify opds. with tat binding.
XX Disclosure; Fig 18c; 89pp; English.
XX
PS
CC The HIV-1 TAR stem-loop sequence (see AAQ21425) was compared to that from
CC HIV-2 (see AAQ21426). The only regions common to the two TAR structures
CC are in the loop region and the U-rich bubble in the upper stem. This 17-
CC mer was synthesised and can hybridise to a 14-mer (see AAQ24061) to mimic
CC the known HIV-1 tat recognition sequence but without the apical loop. In
CC an assay, the 17-mer plus 14-mer structure competed satisfactorily with
CC full-length (59-mer) TAR for binding to tat. See AAQ21427-Q21435 for TAR
CC mutants

SQ Sequence 17 BP; 5 A; 4 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 46.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 9;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1490 AGCCGACTCTCGAGC 1506
DB 1 AGCCGAGUUGAGCAGC 17

RESULT 2
ID AAZ59070 standard; RNA, 17 BP.
AC AAZ59070;
15-SEP-2003 (revised)
DT 11-APR-2000 (first entry)

DE HIV-1 TAR oligonucleotide target sequence #1.

XX Antiviral; antibacterial; antifungal; anticancer; detection; TAR; RRE;
KW fluorescence resonance energy transfer; tat; HIV-1; Rev response element;
KW autoimmune disease; trans-activation regulatory region; ss.
XX Human immunodeficiency virus 1.
OS W09964625-A2.
XX PN 16-DEC-1999.
XX PD 04-JUN-1999; 99MO-GB001761.
XX PF 05-JUN-1998; 98GB-00012196.
XX PR 02-MAR-1999; 99GB-00004790.
XX PA (RIBO-) RIBOTARGETS LTD.
XX PI Karn J, Prescott CD;
XX WPI, 2000-097545/08.
XX DR
XX Identifying compounds that bind to target RNA, potentially useful for
PT treating infections, tumors and autoimmune diseases.
XX Example; Page 31; 82pp; English.
XX The invention relates to a method of determining if a compound binds to a
CC target RNA by treating a test compound with a reporter (R) labelled with a
CC a donor or acceptor group and labelled target RNA, labelled with the
CC complementary donor or acceptor group, and measuring the fluorescence
CC from fluorescent groups associated with a compound:target RNA complex in
CC presence of the test compound and comparing the result with a standard.

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2004, 16:33:22 ; Search time 0.001 Seconds

(without alignments)
79,200 Million cell updates/sec

Title: us-09-954-556-3

Perfect score: 30

Sequence: 1 cagcaccagaagccagactccagcagcca 30

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 0.5

Searched: 102 segs, 1320 residues

Total number of hits satisfying chosen parameters: 204

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 102 summaries

Database: rge.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	14.4	48.0	17	1	AR048076
2	14.4	48.0	17	1	AR048079
3	14.4	48.0	17	1	AR108979
4	14.4	48.0	17	1	AR108982
5	14.4	48.0	18	1	AR048082
6	14.4	48.0	18	1	AR108985
7	13.8	46.0	17	1	A20708
8	13.8	46.0	17	1	A21027
9	13.8	46.0	17	1	BD249433
10	13.8	46.0	17	1	AR340497
11	13.8	46.0	17	1	AX008727
12	13.8	46.0	17	1	AX325661
13	13.8	46.0	17	1	AX325662
14	13.8	46.0	18	1	A21030
15	13.8	46.0	18	1	AR048072
16	13.8	46.0	18	1	AR108975
17	13.8	46.0	18	1	BD249435
18	13.8	46.0	18	1	AR340495
19	13.8	46.0	18	1	AX008729
20	13.8	46.0	18	1	AX084246
21	13.8	46.0	18	1	AX084249
22	12.8	42.7	17	1	AR048077
23	12.8	42.7	17	1	AR048078
24	12.8	42.7	17	1	AR048080
25	12.8	42.7	17	1	AR048081
26	12.8	42.7	17	1	AR108980
27	12.8	42.7	17	1	AR108981
28	12.8	42.7	17	1	AR108984
29	12.8	42.7	17	1	AR108983
30	12.8	40.0	14	1	BD209410
31	12.8	40.0	15	1	A12791
32	11.4	38.0	15	1	ACCESSTION:127893
33	11.4	36.7	14	1	ACCESSTION:A89566

34	11	36.7	14	1	A89567	ACCESSTION:A89567
35	11	36.7	14	1	BD067079	ACCESSTION:BD067079
36	11	36.7	14	1	BD067080	ACCESSTION:BD067080
37	10.8	36.0	14	1	BD209394	ACCESSTION:BD209394
38	10	33.3	10	1	BD239909	ACCESSTION:BD239909
39	10	33.3	12	1	A71513	ACCESSTION:A71513
40	10	33.3	13	1	AX003113	ACCESSTION:AX003113
41	9.4	31.3	11	1	AX623670	ACCESSTION:AX623670
42	9.4	31.3	11	1	AX629388	ACCESSTION:AX629388
43	9.4	31.3	11	1	AX629909	ACCESSTION:AX629909
44	9.4	31.3	11	1	AX630102	ACCESSTION:AX630102
45	9.4	31.3	11	1	AX631091	ACCESSTION:AX631091
46	9.4	31.3	12	1	AR167701	ACCESSTION:AR167701
47	9.4	31.3	12	1	E29585	ACCESSTION:E29585
48	9.4	31.3	12	1	E38691	ACCESSTION:E38691
49	9.4	31.3	12	1	E64117	ACCESSTION:E64117
50	9.4	31.3	12	1	BD061483	ACCESSTION:BD061483
51	9.4	31.3	12	1	BD101930	ACCESSTION:BD101930
52	9	30.0	10	1	BD240229	ACCESSTION:BD240229
53	9	30.0	10	1	BD248497	ACCESSTION:BD248497
54	9	30.0	10	1	AR303300	ACCESSTION:AR303300
55	9	30.0	10	1	AX510716	ACCESSTION:AX510716
56	9	30.0	11	1	AX471386	ACCESSTION:AX471386
57	9	30.0	11	1	AX625231	ACCESSTION:AX625231
58	9	30.0	11	1	AX626985	ACCESSTION:AX626985
59	9	30.0	11	1	AX628452	ACCESSTION:AX628452
60	9	30.0	11	1	AX630058	ACCESSTION:AX630058
61	9	30.0	11	1	AX632652	ACCESSTION:AX632652
62	8.4	28.0	10	1	AR070986	ACCESSTION:AR070986
63	8.4	28.0	10	1	AR161933	ACCESSTION:AR161933
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65	8.4	28.0	10	1	E54684	ACCESSTION:E54684
66	8.4	28.0	10	1	AR181983	ACCESSTION:AR181983
67	8.4	28.0	10	1	AR303303	ACCESSTION:AR303303
68	8.4	28.0	10	1	AR303338	ACCESSTION:AR303338
69	8.4	28.0	10	1	AR304485	ACCESSTION:AR304485
70	8.4	28.0	10	1	AR382219	ACCESSTION:AR382219
71	8.4	28.0	10	1	AX152226	ACCESSTION:AX152226
72	8.4	28.0	10	1	AX152377	ACCESSTION:AX152377
73	8.4	28.0	10	1	AX153162	ACCESSTION:AX153162
74	8.4	28.0	10	1	AX362608	ACCESSTION:AX362608
75	8.4	28.0	10	1	AX373325	ACCESSTION:AX373325
76	8.4	28.0	10	1	BD065117	ACCESSTION:BD065117
77	8.4	28.0	10	1	BD167088	ACCESSTION:BD167088
78	8.4	28.0	11	1	A02163	ACCESSTION:A02163
79	8.4	28.0	11	1	A04685	ACCESSTION:A04685
80	8.4	28.0	11	1	AR030153	ACCESSTION:AR030153
81	8.4	28.0	11	1	AR353840	ACCESSTION:AR353840
82	8.4	28.0	11	1	AX470484	ACCESSTION:AX470484
83	8.4	28.0	11	1	AX470732	ACCESSTION:AX470732
84	8.4	28.0	11	1	AX471384	ACCESSTION:AX471384
85	8.4	28.0	11	1	AX616455	ACCESSTION:AX616455
86	8.4	28.0	11	1	AX624591	ACCESSTION:AX624591
87	8.4	28.0	11	1	AX625489	ACCESSTION:AX625489
88	8.4	28.0	11	1	AX625964	ACCESSTION:AX625964
89	8.4	28.0	11	1	AX626847	ACCESSTION:AX626847
90	8.4	28.0	11	1	AX627093	ACCESSTION:AX627093
91	8.4	28.0	11	1	AX627287	ACCESSTION:AX627287
92	8.4	28.0	11	1	AX627505	ACCESSTION:AX627505
93	8.4	28.0	11	1	AX627654	ACCESSTION:AX627654
94	8.4	28.0	11	1	AX627926	ACCESSTION:AX627926
95	8.4	28.0	11	1	AX628508	ACCESSTION:AX628508
96	8.4	28.0	11	1	AX629116	ACCESSTION:AX629116
97	8.4	28.0	11	1	AX629158	ACCESSTION:AX629158
98	8.4	28.0	11	1	AX629366	ACCESSTION:AX629366
99	8.4	28.0	11	1	AX629825	ACCESSTION:AX629825
100	8.4	28.0	11	1	AX629827	ACCESSTION:AX629827
101	8.4	28.0	11	1	AX630195	ACCESSTION:AX630195
102	8.4	28.0	11	1	AX632012	ACCESSTION:AX632012

ALIGNMENTS